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Rapid analysis of CpG methylation patterns using RNase T1 cleavage and MALDI-TOF

P Schatz, D Dietrich, M Schuster - Nucleic Acids Research, 2004 - Oxford Univ Press

... DNA preparation **Methylated** DNA for the experiment described in Figure 2 was prepared by treating human genomic DNA (Promega) with SssI methyltransferase (New England ... **Unmethylated** DNA was prepared by MDA (**multiple displacement amplification**), a genome-wide ...

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Multiple displacement amplification to create a long-lasting source of DNA for genetic studies

L Lovmar, AC Syvänen - Human mutation, 2006 - interscience.wiley.com

... **Multiple Displacement Amplification To Create ...** The **multiple displacement amplification** (MDA) method, which relies on isothermal amplification using the DNA polymerase of the bacteriophage U29, is a recently developed technique for high performance WGA. ...

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[PDF] Whole genome amplification of sodium bisulfite-treated DNA allows the accurate estimate of methylated cytosine density in limited DNA resources

J Mir, SY Yazdianpanah, E Guckel, S Ziegler, Z ... - ..., 2006 - biotechniques.com

... age of **methylated** cytosines, and red bars denote the percentage of **unmethylated** cytosines at this CpG site. B, non-WGA bisulfite-treated DNA; P, PEP-amplified bisulfite-treated DNA; R, bi-sulfite-treated DNA amplified with the REPLI-g **multiple displacement amplification** (MDA) ...

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[biotechniques.com \[PDF\]](#)

Analysis of repetitive element DNA methylation by MethylLight

DJ Weisenberger, M Campan, TJ Long, M ... - Nucleic acids ..., 2005 - Oxford Univ Press

... Here, we report the development of quantitative MethylLight assays to determine the levels of **methylated** and **unmethylated** repeats, namely, Alu and LINE-1 sequences and the centromeric satellite alpha (Sat) and juxtacentromeric satellite 2 (Sat2) DNA sequences. ...

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Novel method for high throughput DNA methylation marker evaluation using PNA-probe library hybridization and MALDI-TOF detection

P Schatz, J Distler, K Berlin, M Schuster - Nucleic acids research, 2006 - Oxford Univ Press

... **Unmethylated** DNA was prepared by MDA (**multiple displacement amplification**), a genome-wide amplification method described by Dean et al. (30). **Methylated** DNA was prepared by treating **unmethylated** MDA-DNA with SssI methyltransferase (New England Biolabs, Frankfurt ...

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Analysis of DNA methylation of multiple genes in microdissected cells from formalin-fixed and paraffin-embedded tissues

D Dietrich, R Lesche, R Tetzner, M ... - Journal of ..., 2009 - Histochemical Soc

... **Unmethylated** DNA was prepared by **multiple displacement amplification** (MDA), a genome-wide amplification method (Dean et al. ... A measurement originating only from a few copies might not reflect the actual representation of **methylated** and **unmethylated** copies. ...

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[PDF] Characterizing the physical genome

JR Pollack, VR Iyer - nature genetics, 2002 - stanford.edu

... Oligonucleotide arrays have also shown promise in directly discriminating **methylated** from **unmethylated** CpG dinu- cleotides31,32. Bisulphite modification of genomic DNA converts **unmethylated** cytosines, but not **methylated** cytosines, to uracil. ...

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[stanford.edu \[PDF\]](#)

[HTML] The use of multiple displacement amplified DNA as a control for methylation specific PCR, pyrosequencing, bisulfite sequencing and methylation-sensitive ...

S Hughes, JT Jones - BMC molecular biology, 2007 - biomedcentral.com

... To enable this, suitable control DNA samples are required that correspond to fully CpG **unmethylated** and fully CpG **methylated** DNA. ... presented here use a combination of whole genome amplification (WGA) using the **multiple displacement amplification** (MDA) approach [11 ...

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[PDF] Authentication of forensic DNA samples

D Frumkin, A Wasserstrom, A Davidson, A ... - Forensic Science ..., 2010 - nucleix.com

... In the human genome 70–80% of all CpGs are **methylated**, while **unmethylated** CpGs are grouped in ... WGA: Whole genome amplification was performed by **multiple displacement amplification** [16] with the Repli-g Midi kit (QIAGEN) using 10 ng of natural DNA as template. ...

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Simple screening method for differentially **methylated** regions of the genome using a small number of cells

T Hamada, S Murasawa, T Asahara - Biochemical and biophysical ..., 2007 - Elsevier